KW

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/763,535

DATE: 08/01/2001
TIME: 18:42:56

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF3\08012001\I763535.raw**

```
 4 <110> APPLICANT: UNIVERSITE CATHOLIQUE DE LOUVAIN
 5        ROUSSEAU, GUY
 6        LEMAIGRE, FREDRIC
 8 <120> TITLE OF INVENTION: PHARMACEAUTICLA COMPOSITION FOR TREATING
 9        OR PREVENTING DIABETES OR CANCER, OR THE WAARDENBURG
10        SYNDROME
12 <130> FILE REFERENCE: DECLE26.001APC
14 <140> CURRENT APPLICATION NUMBER: US 09/763,535
15 <141> CURRENT FILING DATE: 2001-02-20
17 <150> PRIOR APPLICATION NUMBER: BE 9800609
18 <151> PRIOR FILING DATE: 1998-08-17
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1655
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1
30 gcccccgccc gccccgggcc ctgatggact gaatgaaggc tgcctacacc gcctatcgat 60
31 gcctcaccaa agacctagaa cgtgcgccat gaacccggag ctgacaatgg aaagtctggg 120
32 cactttgcac ggcgcgcgcg gcggcggcag tggcggggdc ggcggcgggg gcggcggggg 180
33 cggcggcggg ggcccgggcc atgagcagga gctgctggcc agccccagcc cccaccacgc 240
34 gcgccgcggc ccgcgtggct cgctgcgggg ccctccgccg cctccaaccg cgcaccagga 300
35 gctgggcacg gcggcagcgg cggcagcggc ggcgtcgcgc tcggccatgg tcaccagcat 360
36 ggcctcgatc ctggacggcg gcgactaccg gcccgagctc tccatcccgc tgcaccacgc 420
37 catgagcatg tcctgcgact cgtctccgcc tggcatgggc atgagcaaca cctacaccac 480
38 gctgacaccg ctccagccgc tgccacccat ctccaccgtg tctgacaagt tccaccaccc 540
39 tcacccgcac caccatccgc accaccacca ccaccaccac caccagcgcc tgtccggcaa 600
40 cgtcagcggc agcttcaccc tcatgcgcga cgagcgcggg ctcccggcca tgaacaacct 660
41 ctacagtccc tacaaggaga tgcccggcat gagccagagc ctgtccccgc tggccgccac 720
42 gccgctgggc aacgggctag gcggcctcca caacgcgcag cagagtctgc ccaactacgg 780
43 tccgccgggc cacgacaaaa tgctcagccc caacttcgac gcgcaccaca ctgccatgct 840
44 gacccgcggt gagcaacacc tgtcccgcgg cctgggcacc ccacctgcgg ccatgatgtc 900
45 gcacctgaac ggcctgcacc acccgggcca cactcagtct cacgggccgg tgctggcacc 960
46 cagtcgcgag cggccaccct cgtcctcatc gggctcgcag gtggccacgt cgggccagct 1020
47 ggaagaaatc aacaccaaag aggtggccca gcgcatcaca gcggagctga agcgctacag 1080
48 tatcccccag gcgatctttg cgcagagggt gctgtgccgg tctcagggga ctctctccga 1140
49 cctgctccgg aatccaaaac cgtggagtaa actcaaatct ggcagggaga ccttccgcag 1200
50 gatgtggaag tggcttcagg agcccgagtt ccagcgcatg tccgccttac gcctggcagc 1260
51 gtgcaaacgc aaagagcaag aaccaaacaa agacaggaac aattcccaga agaagtcccg 1320
52 cctggtgttc actgacctcc aacgccgaac actcttcgcc atcttcaagg agaacaaacg 1380
53 cccgtcaaag gagatgcaga tcaccatttc ccagcagctg ggcctggagc tcacaaccgt 1440
54 cagcaacttc ttcatgaacg cccggcgccg cagcctggag aagtggcaag acgatctgag 1500
55 cacagggggc tcctcgtcca cctccagcac gtgtaccaaa gcatgatgga aggactctca 1560
56 cttgggcaca agtcacctcc aaatgaggac aacagatacc aaaagaaaac aaaggaaaaa 1620
57 gacaccggat tcctagctgg ggcccttcac tggtg         1655
59 <210> SEQ ID NO: 2
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 60 <211> LENGTH: 485
 61 <212> TYPE: PRT
 62 <213> ORGANISM: Homo sapiens
 64 <400> SEQUENCE: 2
 65 Met Asn Pro Glu Leu Thr Met Glu Ser Leu Gly Thr Leu His Gly Ala
 66 1               5                   10                  15
 67 Arg Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 68             20                  25                  30
 69 Gly Gly Gly Pro Gly His Glu Gln Glu Leu Leu Ala Ser Pro Ser Pro
 70         35                  40                  45
 71 His His Ala Arg Arg Gly Pro Arg Gly Ser Leu Arg Gly Pro Pro Pro
 72     50                  55                  60
 73 Pro Pro Thr Ala His Gln Glu Leu Gly Thr Ala Ala Ala Ala Ala Ala
 74 65                  70                  75                  80
 75 Ala Ala Ser Arg Ser Ala Met Val Thr Ser Met Ala Ser Ile Leu Asp
 76             85                  90                  95
 77 Gly Gly Asp Tyr Arg Pro Glu Leu Ser Ile Pro Leu His His Ala Met
 78             100                 105                 110
 79 Ser Met Ser Cys Asp Ser Ser Pro Pro Gly Met Gly Met Ser Asn Thr
 80         115                 120                 125
 81 Tyr Thr Thr Leu Thr Pro Leu Gln Pro Leu Pro Pro Ile Ser Thr Val
 82     130                 135                 140
 83 Ser Asp Lys Phe His His Pro His Pro His His His Pro His His His
 84 145                 150                 155                 160
 85 His His His His His Gln Arg Leu Ser Gly Asn Val Ser Gly Ser Phe
 86             165                 170                 175
 87 Thr Leu Met Arg Asp Glu Arg Gly Leu Pro Ala Met Asn Asn Leu Tyr
 88             180                 185                 190
 89 Ser Pro Tyr Lys Glu Met Pro Gly Met Ser Gln Ser Leu Ser Pro Leu
 90         195                 200                 205
 91 Ala Ala Thr Pro Leu Gly Asn Gly Leu Gly Gly Leu His Asn Ala Gln
 92     210                 215                 220
 93 Gln Ser Leu Pro Asn Tyr Gly Pro Pro Gly His Asp Lys Met Leu Ser
 94 225                 230                 235                 240
 95 Pro Asn Phe Asp Ala His His Thr Ala Met Leu Thr Arg Gly Glu Gln
 96             245                 250                 255
 97 His Leu Ser Arg Gly Leu Gly Thr Pro Pro Ala Ala Met Met Ser His
 98             260                 265                 270
 99 Leu Asn Gly Leu His His Pro Gly His Thr Gln Ser His Gly Pro Val
100         275                 280                 285
101 Leu Ala Pro Ser Arg Glu Arg Pro Pro Ser Ser Ser Ser Gly Ser Gln
102     290                 295                 300
103 Val Ala Thr Ser Gly Gln Leu Glu Glu Ile Asn Thr Lys Glu Val Ala
104 305                 310                 315                 320
105 Gln Arg Ile Thr Ala Glu Leu Lys Arg Tyr Ser Ile Pro Gln Ala Ile
106             325                 330                 335
107 Phe Ala Gln Arg Val Leu Cys Arg Ser Gln Gly Thr Leu Ser Asp Leu
108             340                 345                 350
109 Leu Arg Asn Pro Lys Pro Trp Ser Lys Leu Lys Ser Gly Arg Glu Thr
```

```
110         355                 360                 365
111 Phe Arg Arg Met Trp Lys Trp Leu Gln Glu Pro Glu Phe Gln Arg Met
112     370                 375                 380
113 Ser Ala Leu Arg Leu Ala Ala Cys Lys Arg Lys Glu Gln Glu Pro Asn
114 385                 390                 395                 400
115 Lys Asp Arg Asn Asn Ser Gln Lys Lys Ser Arg Leu Val Phe Thr Asp
116                 405                 410                 415
117 Leu Gln Arg Arg Thr Leu Phe Ala Ile Phe Lys Glu Asn Lys Arg Pro
118             420                 425                 430
119 Ser Lys Glu Met Gln Ile Thr Ile Ser Gln Gln Leu Gly Leu Glu Leu
120         435                 440                 445
121 Thr Thr Val Ser Asn Phe Phe Met Asn Ala Arg Arg Arg Ser Leu Glu
122     450                 455                 460
123 Lys Trp Gln Asp Asp Leu Ser Thr Gly Gly Ser Ser Ser Thr Ser Ser
124 465                 470                 475                 480
125 Thr Cys Thr Lys Ala
126                 485
129 <210> SEQ ID NO: 3
130 <211> LENGTH: 1485
131 <212> TYPE: DNA
132 <213> ORGANISM: Homo sapiens
134 <400> SEQUENCE: 3
135 atggagctga gcctggagag cctggggggc ctgcacagcg tggcccacgc gcaggcgggc 60
136 gagctgctga gcccgggcca cgcgcgctcg gcggcggcgc agcaccgcgg cctggtggcg 120
137 cccgggcgcc cgggcctggt ggccggcatg gcgagcctgc tggacggcgg cggcggcggc 180
138 ggcggtgggg gcgccggggg cgcgggcggc gcgggcagcg cgggcggcgg cgcggacttc 240
139 cgcggggaac tggcgggccc gctgcacccg gcaatgggca tggcctgcga ggcgccgggc 300
140 ctgggcggca cctacgacgc gctcacgccc ctgcagcacc tgccgccgct cgcggccgtg 360
141 gccgacaagt tccaccagca cgcggcggcc gcggccgtgg ccggggcgca cggcggccat 420
142 ccccacgcgc acccgcaccc ggcggccgcg ccgcccccgc cacccccgcc gcagcgtctg 480
143 gcggccagcg tgagcggcag cttcaccctc atgcgcgacg agcggggcggc gctcgcctcc 540
144 gtgggccacc tctacggacc ctacggcaag gagctgcccg ccatggggtc gccgctgtcg 600
145 ccgctgccca acgcgctgcc gcccgcgctg cacggcgccc cgcagccccc gccgccgcca 660
146 ccaccccccgc cgctggccgc ctacggcccg ccaggccacc tggctgggga caagctgctg 720
147 ccgcccgccg ccttcgagcc gcacgccgcg ctgctgggac gcgcggagga cgcactggcc 780
148 cgcgggctgc ccggaggcgg cggcggcaca ggcagcggcg gagcgggcag cgggagcgcc 840
149 gcggggctgc tggcgccgct gggcgggctg gcggcggccg gggcgcacgg gccgcacggg 900
150 ggaggcggcg gccccggcgg gagcggcggc ggccccagcg cgggcgcagc ggccgaggag 960
151 atcaacacca aggaggtggc gcagcgcatc acggcggagc tgaagcgcta cagcatcccg 1020
152 caggcaatct tcgcgcagcg gatcctgtgt cgctctcagg gcacgctctc cgacctgctg 1080
153 cgcaacccca agccgtggag caagctcaaa tccggccgcg agaccttccg caggatgtgg 1140
154 aagtggctgc aggagccaga gttccagcgc atgtcggcgc tgcgcttggc agcgtgcaag 1200
155 cgcaaggaac aggagcagca gaaggagcgc gccctgcagc ccaagaagca gcgcctggtg 1260
156 ttcaccgacc tgcagcgacg cacgctgatc gccatcttca aggagaacaa gcggccgtcc 1320
157 aaggagatgc aggtcaccat ctcgcagcag ctcggcttgg agctcaacac cgtcagcaac 1380
158 ttcttcatga cgcgcggcg ccgctgcatg aaccgctggg ctgaggagcc cagcacggcc 1440
159 cccgggggcc ccgccggcgc cacggccact ttctccaagg cctga 1485
161 <210> SEQ ID NO: 4
162 <211> LENGTH: 494
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163 <212> TYPE: PRT
164 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 4
167 Met Glu Leu Ser Leu Glu Ser Leu Gly Gly Leu His Ser Val Ala His
168  1               5                  10                  15
169 Ala Gln Ala Gly Glu Leu Leu Ser Pro Gly His Ala Arg Ser Ala Ala
170             20                  25                  30
171 Ala Gln His Arg Gly Leu Val Ala Pro Gly Arg Pro Gly Leu Val Ala
172         35                  40                  45
173 Gly Met Ala Ser Leu Leu Asp Gly Gly Gly Gly Gly Gly Gly Gly Gly
174     50                  55                  60
175 Ala Gly Gly Ala Gly Gly Ala Gly Ser Ala Gly Gly Gly Ala Asp Phe
176 65                  70                  75                  80
177 Arg Gly Glu Leu Ala Gly Pro Leu His Pro Ala Met Gly Met Ala Cys
178             85                  90                  95
179 Glu Ala Pro Gly Leu Gly Gly Thr Tyr Thr Thr Leu Thr Pro Leu Gln
180             100                 105                 110
181 His Leu Pro Pro Leu Ala Ala Val Ala Asp Lys Phe His Gln His Ala
182         115                 120                 125
183 Ala Ala Ala Ala Val Ala Gly Ala His Gly Gly His Pro His Ala His
184     130                 135                 140
185 Pro His Pro Ala Ala Ala Pro Pro Pro Pro Pro Pro Gln Arg Leu
186 145                 150                 155                 160
187 Ala Ala Ser Val Ser Gly Ser Phe Thr Leu Met Arg Asp Glu Arg Ala
188             165                 170                 175
189 Ala Leu Ala Ser Val Gly His Leu Tyr Gly Pro Tyr Gly Lys Glu Leu
190             180                 185                 190
191 Pro Ala Met Gly Ser Pro Leu Ser Pro Leu Pro Asn Ala Leu Pro Pro
192         195                 200                 205
193 Ala Leu His Gly Ala Pro Gln Pro Pro Pro Pro Pro Pro Pro Pro Pro
194     210                 215                 220
195 Leu Ala Ala Tyr Gly Pro Pro Gly His Leu Ala Gly Asp Lys Leu Leu
196 225                 230                 235                 240
197 Pro Pro Ala Ala Phe Glu Pro His Ala Ala Leu Leu Gly Arg Ala Glu
198             245                 250                 255
199 Asp Ala Leu Ala Arg Gly Leu Pro Gly Gly Gly Gly Thr Gly Ser
200             260                 265                 270
201 Gly Gly Ala Gly Ser Gly Ser Ala Ala Gly Leu Leu Ala Pro Leu Gly
202     275                 280                 285
203 Gly Leu Ala Ala Ala Gly Ala His Gly Pro His Gly Gly Gly Gly Gly
204     290                 295                 300
205 Pro Gly Gly Ser Gly Gly Gly Pro Ser Ala Gly Ala Ala Ala Glu Glu
206 305                 310                 315                 320
207 Ile Asn Thr Lys Glu Val Ala Gln Arg Ile Thr Ala Glu Leu Lys Arg
208             325                 330                 335
209 Tyr Ser Ile Pro Gln Ala Ile Phe Ala Gln Arg Ile Leu Cys Arg Ser
210             340                 345                 350
211 Gln Gly Thr Leu Ser Asp Leu Leu Arg Asn Pro Lys Pro Trp Ser Lys
212     355                 360                 365
```

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```
213 Leu Lys Ser Gly Arg Glu Thr Phe Arg Arg Met Trp Lys Trp Leu Gln
214     370             375             380
215 Glu Pro Glu Phe Gln Arg Met Ser Ala Leu Arg Leu Ala Ala Cys Lys
216 385             390             395             400
217 Arg Lys Glu Gln Glu Gln Gln Lys Glu Arg Ala Leu Gln Pro Lys Lys
218             405             410             415
219 Gln Arg Leu Val Phe Thr Asp Leu Gln Arg Arg Thr Leu Ile Ala Ile
220         420             425             430
221 Phe Lys Glu Asn Lys Arg Pro Ser Lys Glu Met Gln Val Thr Ile Ser
222     435             440             445
223 Gln Gln Leu Gly Leu Glu Leu Asn Thr Val Ser Asn Phe Phe Met Asn
224     450             455             460
225 Ala Arg Arg Arg Cys Met Asn Arg Trp Ala Glu Glu Pro Ser Thr Ala
226 465             470             475             480
227 Pro Gly Gly Pro Ala Gly Ala Thr Ala Thr Phe Ser Lys Ala
228             485             490
```

VERIFICATION SUMMARY   DATE: 08/01/2001
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Output Set: **N:\CRF3\08012001\I763535.raw**